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54 **Human DNA in the diagnosis of retinoblastoma.**

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Description

This invention relates to methods of detection and treatment of a defective human gene related to cancer, in particular, retinoblastoma.

Nature 305 (1983) 779-84 discloses that a mutation at the retinoblastoma locus (Rb-1), mapped to human chromosome 13 band q14, results in a predisposition to retinoblastoma.

Retinoblastoma is a neoplastic condition of the retinal cells, observed almost exclusively in children between the ages of 0 and 4 years. If untreated, the malignant neoplastic retinal cells in the intraocular tumor travel to other parts of the body, forming foci of uncontrolled growth which are always fatal. The current treatment for a retinoblastoma is enucleation of the affected eye if the intraocular tumor is large; for small intraocular tumors, radiation therapy, laser therapy, or cryotherapy is preferred. There is no known successful treatment for metastatic retinoblastoma. Hence, early diagnosis of retinoblastoma to allow treatment before the tumor spreads outside the eye is crucial.

There is evidence that retinoblastoma is caused by the functional loss of both homologous copies of the retinoblastoma (Rb) gene. Thus, individuals carrying one defective allele of the Rb gene are genetically predisposed to the disease. Children who have had one eye affected by retinoblastoma or who are related to someone with retinoblastoma may be genetically predisposed and therefore at risk of developing the disease. These individuals routinely are tested for retinoblastoma every 2-3 months by an ocular examination procedure which requires placing the child under general anesthesia.

The invention relates to the use of genetic material corresponding to a normal human retinoblastoma gene or a unique subregion thereof in the preparation of material for use in a method of screening human patients comprising comparing the DNA of said patients with the said gene or subregion. Also encompassed are vectors comprising genetic material corresponding to a normal retinoblastoma gene, or a unique subregion thereof.

In general, the invention features a method of screening human patients by comparing the DNA of these patients with the isolated normal human retinoblastoma (Rb) gene or a unique subregion thereof (the term "unique subregion" means a DNA sequence found in the Rb gene and not elsewhere in the human genome). This comparison allows detection of defective Rb alleles in the patients, to determine whether these patients need continual monitoring by the conventional examination procedure. More importantly, this comparison will identify those patients who do not have a defective Rb

allele and thus are not at risk of developing retinoblastoma and do not have to be examined by the conventional procedure.

Preferably, the comparison between the patient's DNA and the normal Rb gene involves testing the patient's DNA with the isolated Rb gene to detect either large deletions or, alternatively, small deletions or point mutations in the Rb locus. To test for large deletions in a patient's Rb allele, the patient's DNA preferably is analyzed by DNA hybridization using probes made from the isolated normal Rb gene. According to the invention, small deletions or point mutations preferably are detected by either of two techniques. The nucleotide sequences of the patients' Rb alleles and the normal Rb gene can be determined and compared for differences. Alternatively, the patient's DNA is probed with the normal Rb gene and any mismatches in the resulting heteroduplexes are identified.

Also, the isolated normal human retinoblastoma gene can be used to produce the normal Rb gene product for protein therapy of individuals determined to have a defective Rb allele.

In another aspect, the invention features a method of detecting the presence, in a tumor sample, of a retinoblastoma protein the absence of which is associated with a distinct set of neoplasms. The method comprises producing an antibody to the Rb protein, contacting the antibody with the tumor sample, and detecting immune complexes as an indication of the presence of the protein in the tumor sample. If a tumor lacks the Rb gene product, no immune complexes will be found, and one may conclude that the tumor was the result of mutant Rb alleles. This limits the pathologic diagnosis to those tumors known to be caused by mutant Rb alleles, such as retinoblastoma, osteosarcoma, and some undifferentiated tumors of unknown cellular origin. A more exact categorization of pathologic diagnosis of human tumors will result.

Description of the Preferred Embodiments

The drawings first will be briefly described.

Drawings

Fig. 1 is a pictorial representation of the autoradiogram from a Northern blot probed with p7H30.7R;

Fig. 2 is a diagrammatic representation of the restriction map of the insert in the clone p4.7R;

Fig 3 is a pictorial representation of the autoradiogram from a Northern blot probed with p4.7R;

Fig. 4 is a diagrammatic representation of the vectors p2AR3.8 and p2AR0.9 of the invention;

Fig. 5 is a diagrammatic representation of the mismatch detection technique;

Fig. 6 is a diagrammatic representation of an example denaturing gel used in mismatch detection.

Fig. 7 is the sequence of the normal Rb gene, with flanking regions.

Isolation of the Normal Rb Gene

The genetic locus involved in causing retinoblastoma has been assigned to the q14 band of human chromosome 13 (Sparkes et al., *Science* 208:1042 (1980). A cDNA clone, p4.7R, from this region of DNA has been shown to carry Rb gene sequences. This clone was obtained by the following general techniques.

Isolation of cDNA Clone p4.7R

The human DNA probe pH3-8, isolated from a human chromosome 13 lambda phage library (Lalande et al., 1984, *Cancer Genet. Cytogenet.* 13:283), was used in a chromosome walking technique to isolate and map 30 kb of genomic DNA surrounding the H3-8 sequence. One fragment generated by this technique, named p7H30.7R, was found to recognize a DNA sequence in the mouse genome as well as within human chromosome 13 (Dryja et al., 1986, *Proc. Nat. Acad. Sci. USA* in press). The homology of p7H30.7R to both human and mouse DNA suggested that p7H30.7R contained coding sequences of a structural gene.

To test this possibility, p7H30.7R was radiolabeled and used to probe a Northern blot of RNA isolated from three retinoblastoma tumors (#42, #30, and #31) and an adenovirus 12-transformed human embryonic retinal cell line (Ret) (Vaessen et al., 1986, *EMBO Journal* 5:335). The p7H30.7R probe hybridized to an RNA transcript of approximately 4.7 kb from the retinal cell line, but did not hybridize to any RNA transcripts from the three tumor samples (Fig. 1).

Subsequently, RNA isolated from the adenovirus-transformed retinal cell line was used to construct a cDNA library. This library was screened with the labeled p7H30.7R probe. Several cDNA clones were isolated which had similar restriction maps. The longest of these, p4.7R, contained 4.7 kb of genomic DNA. The physical map of p4.7R is shown in Fig. 2.

Characterization of p4.7R

The p4.7R clone was used to screen RNA transcripts isolated from retinoblastomas (#42, #30, #41, #31), an osteosarcoma (#16), and the adenovirus-transformed retinal cells (Ret). As shown in Fig. 3, the p4.7R probe detected, in a Northern blot analysis of isolated RNA's, a transcript in the transformed retinal cells which is not present in the four retinoblastoma and one osteosarcoma cell samples. The bands at ~ 2.0 kb were detected by reprobing the Northern blot, after washing, with a probe that detects rat tubulin (to demonstrate the presence of RNA in the blot).

The p4.7R clone also was used to screen genomic DNA. DNA was isolated from a set of tumors from 50 unrelated individuals, consisting of 40 retinoblastomas, 8 osteosarcomas, and 2 undifferentiated tumors of unknown cellular origin arising in patients with hereditary retinoblastoma. The isolated samples of DNA were digested with HindIII and analyzed by Southern blot hybridization using radiolabeled p4.7R as the probe. This analysis revealed three types of deviant patterns of the genomic DNA restriction fragments: totally absent fragments, representing apparent homozygous deletions; under-represented fragments, representing apparent heterozygous deletions; and fragments of altered size, reflecting either partial deletion or an alteration of a restriction site. At least 30% of the tumor DNA's exhibited one of these abnormalities. In comparison, Southern blot analysis of leukocyte DNA from 18 normal individuals showed a uniform pattern of restriction fragments.

The above results indicate that p4.7R detects the Rb gene. The deletion pattern in one osteosarcoma DNA sample provided particularly good evidence that p4.7R detects the Rb gene. This DNA sample is homozygous for a deletion that maps entirely within the p4.7R region. It is highly unlikely that the osteosarcoma phenotype arose due to a mutation independent of this deletion. Since the deletion is limited to the p4.7R region, this region must contain the Rb gene which, when mutated, produces non-functional Rb-encoded protein. The absence of functional Rb protein allows the neoplastic phenotype to develop.

Use

The p4.7R sequences can be used, according to the invention, to screen individuals for the presence of a mutated allele of the Rb gene. This screening procedure will allow individuals having a risk of developing retinoblastoma--because of family history or a previous incidence of retinoblastoma in one eye--to determine the need for routine testing by the cur-

rent ocular examination procedure. Only if the screening procedure determines that the individual possesses a mutant Rb allele will the examination procedure need to be conducted on a regular basis. Those with two normal Rb alleles can discontinue examination, as the risk of developing retinoblastoma in an individual with two normal copies of the Rb gene is approximately 1 in 20,000, or 0.005%, compared to a risk of 80%-90% if an individual has an Rb allele containing a mutation sufficient to inactivate the allele. Thus, a substantial percentage of individuals who are currently examined regularly are not actually at a greater risk than the general population: neither a family history of nor a previous incidence of retinoblastoma is conclusive evidence that an individual has the genetic predisposition to the disease. Therefore, such individuals, actually carrying two normal copies of the Rb gene, have been repeatedly undergoing the expensive and traumatic ocular examination procedure needlessly.

The screening procedure according to the invention preferably can be of two major types: (1) testing an individual's DNA for deletions in the Rb locus large enough to interfere with hybridization to an Rb probe, and (2) testing an individual's DNA for small deletions or point mutations in the Rb locus.

In addition to screening, the invention has the potential to provide protein therapy for those individuals determined to contain a mutant Rb allele and who therefore are at risk of developing retinoblastoma.

An additional use of the invention, as mentioned above, is in immunodiagnosis to determine, for example, whether a certain tumor is the result of an Rb gene abnormality. Since osteosarcomas and certain undifferentiated tumors can result from detectable lesions in the Rb gene, the immunodiagnosis can be used to aid in the diagnosis of such tumors.

Illustrative examples are given below.

Example 1: Southern Blot Analysis

To detect large deletions in the Rb locus, a Southern Blot analysis is carried out on DNA obtained from an individual to be tested. The DNA is obtained from peripheral leucocytes or, if the patient has had a tumor in one eye, from the tumor. To examine leucocyte DNA, a 10 ml blood sample is obtained from the individual, and the genomic DNA is isolated from the leucocytes in the sample, according to standard techniques. This DNA is digested with a restriction endonuclease, e.g., HindIII, run on an agarose electrophoresis gel, and transferred to a nitrocellulose filter by blotting. The DNA on the filter is then probed with radiolabeled

p2AR3.8 and, separately, p2AR0.9, containing subfragments from p4.7R obtained by EcoRI digestion (Fig. 4); it is preferred to use two or more subfragments separately rather than the entire p4.7R insert, in order to better define the location of any abnormalities detected. Autoradiograms of the probed filter give a restriction map of the Rb locus in the somatic or tumor DNA of the tested individual.

This restriction map then is compared with a control restriction map, determined by using the same restriction enzyme digestion and probe. A suitable control can be DNA obtained from the adenovirus-transformed retinal cell line or leucocyte DNA from a set of normal individuals. If the tested individual has an Rb allele containing a significantly large deletion, the above restriction map of his DNA, compared with the control, will contain an additional band or bands, and/or a band or bands that have lost 50% of their intensity, caused by a change in the size, or total elimination, of one or more restriction fragments by the deletion in one allele at the Rb locus.

Thus, this screening procedure by Southern analysis will detect the existence of non-functional Rb alleles which have large deletions. If this analysis indicates that the tested DNA from an individual has a restriction map different from the control map, there is a great probability that the individual contains a non-functional, mutant Rb allele. The individual must be monitored closely thereafter for the development of retinoblastoma.

If the test restriction map appears identical to the control, a different screening procedure can be performed on the individual's DNA to determine if the individual contains an Rb allele having a small deletion or point mutation, which is sufficient to inactivate the allele but not to prevent hybridization with a probe. This screening procedure is described in the following example.

Example 2: Rb Locus Fine Structural Analysis

To examine an individual's DNA for small deletions or point mutations in the Rb locus, both homologs of the Rb gene from the individual preferably are cloned. The cloned alleles then can be tested for the presence of sequence differences from the normal allele, represented by p4.7R, by one of the following two methods: (1) the nucleotide sequence of both the cloned alleles and p4.7R are determined and then compared, or (2) RNA transcripts from p4.7R are hybridized to single stranded whole genomic DNA from an individual to be tested, and the resulting heteroduplex is treated with RNase A and run on a denaturing gel to detect the location of any mismatches. In more detail, these methods are carried out as follows:

(1) Cloning Rb alleles

The alleles of the Rb gene in an individual to be tested are cloned using conventional techniques. A common method, for example, employs the bacteriophage vector EMBL3 (Frischauf et al., 1983, J. Mol. Biol. 170:827). A 10 ml blood sample is obtained from the individual, and the genomic DNA is isolated from the cells in this sample. This DNA is partially digested with *Mbol* to an average fragment size of approximately 20 kb. Fragments in the range from 18-21 kb are isolated. The resulting *Mbol*-ended fragments are ligated into the EMBL3 vector DNA which has been completely digested with *Bam*HI, treated with alkaline phosphatase, and heated to 68°C for 10 minutes to disrupt the cohesive ends. This ligation mix is used in an *in vitro* lambda packaging reaction, and the packaged phage are amplified by growing a plate stock. [This cloning technique is described generally in Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Publications, pp 256-293 (1982).]

Approximately 5×10^5 pfu from this plate stock are used to infect 3 ml of *E. coli* cells at $\sim 1.5 \times 10^9$ cells/ml in 0.01M MgSO_4 , and the infection mix is incubated at 37°C for 20 minutes. 65 ml melted top agar at 47°C is added, and the mixture is plated onto ten 150 mm plates containing freshly poured and dry bottom agar. The agar plates are incubated until the plaques reach a diameter of ~ 1.5 mm and are just beginning to contact one another (approximately 10-12 hours).

Duplicate circular nitrocellulose filters (Millipore™ HAWP) are placed gently on the surface of each agar plate to bind the bacteriophage DNA. The filters are carefully removed after 1 minute, placed into a denaturing solution (1.5M NaCl, 0.5M NaOH) for 30 seconds, neutralized for 5 minutes (1.5M NaCl, 0.5M Tris-Cl pH 8.0), and dried under vacuum at 80°C for 2 hours.

These nitrocellulose filters then are probed with radiolabeled p4.7R by hybridization and autoradiography. Plaques which show hybridization to the p4.7R probe are plaque-purified and rescreened according to the above procedure. Positive plaques from the rescreening are isolated and used to prepare DNA putatively containing Rb alleles from the individual.

The *Mbol* genomic inserts in these isolated EMBL3 vector DNA samples are tested for the location of the sequences homologous to p4.7R by Southern analysis. DNA samples containing the entire Rb gene region are selected, and the appropriate restriction fragments containing the Rb gene from these samples are subcloned into a suitable vector, such as pUC9. These subclones thus contain copies of one or both Rb alleles from the DNA

of the individual to be tested. To determine if both alleles are represented, the initial phage isolates are tested for the existence of restriction polymorphism. These subcloned alleles are then examined for differences from p4.7R by one of the following techniques.

(2) Sequence Comparison

First, the nucleotide sequence of the normal Rb gene in p4.7R is determined by subcloning restriction fragments of ~ 500 bp from p4.7R into an M13mp8 phage vector and sequencing these subclones by the dideoxy technique (Sanger et al., 1977, Proc. Nat. Acad. Sci USA 74:5463). A composite sequence of the Rb gene then can be assembled from these individual subclone sequences. This sequence is given in Fig. 7 which also shows flanking regions.

The isolated Rb gene alleles are sequenced according to the following procedure. Restriction fragments (~ 2 kb) of the allele are subcloned into the M13mp8 vector, and short stretches (~ 500 bp) are sequenced individually using small restriction fragments isolated from p4.7R as the primers in the dideoxy sequencing reactions. The composite nucleotide sequence of the isolated allele then can be constructed from these individually-primed sequences. This sequence is compared directly with the sequence of the normal Rb gene, determined from p4.7R, to determine if any deletions or point mutations exist in the isolated allele.

(3) Ribonuclease Cleavage of Mismatches

An alternative method of comparing the allelic DNA with the normal Rb gene employs RNase A to detect the existence of differences between the p4.7R sequence and the allele sequence. This comparison is performed in steps with small (~ 500 bp) restriction fragments of p4.7R as the probe. First, p4.7R is digested with a restriction enzyme(s) that cuts the Rb gene sequence into fragments of approximately 500bp. These fragments are isolated on an electrophoresis gel and cloned individually, in both orientations, into an SP6 vector, such as pSP64 or pSP65 (Melton et al., 1984, Nucleic Acids Res. 12:7035). The SP6-based plasmids containing inserts of p4.7R fragments are transcribed *in vitro* using the SP6 transcription system, well known in the art, in the presence of $[\alpha\text{-}^{32}\text{P}]\text{GTP}$, generating radiolabeled RNA transcripts of both strands of the cDNA of the Rb gene.

Individually, these RNA transcripts are used to form heteroduplexes with the allelic DNA, as follows. 50 ng of the allele subclone is digested with a restriction enzyme that cuts outside of the region covered by the RNA transcript probe to be used.

This digested DNA is mixed with the radiolabeled RNA probe in 30 μ l of hybridization buffer (80% formamide, 40 mM Pipes pH6.4, 0.4M NaCl, and 1mM EDTA) and the mixture is treated at 90 °C for 10 minutes to denature the DNA. The mixture then is cooled slowly to 45 °C and the RNA is allowed to anneal to the single-stranded DNA at 45 °C for half an hour.

The RNA:DNA heteroduplexes next are treated with 350 μ l of an RNase A solution (Sigma) (40 μ g/ml in 10mM Tris-HCl pH7.5, 1mM EDTA, 0.2M NaCl, and 0.1M LiCl). The mixture is vortexed and incubated at 25 °C for 30 minutes. The RNase A reaction is stopped by adding 10 μ l of proteinase K (10mg/ml) (Boehringer Mannheim) followed by incubation at 37 °C for 20 minutes. Extraction with phenol-chloroform and ethanol precipitation of the aqueous layer yields a nucleic acid sample free from protein contamination. The precipitated sample is resuspended in 5 μ l and analyzed by denaturing polyacrylamide gel electrophoresis (4% polyacrylamide, 7M urea) (Fig. 5).

Mismatches that occur in the RNA:DNA heteroduplex, due to sequence differences between the p4.7R fragment and the Rb allele subclone from the individual, result in cleavage in the RNA strand by the RNase A treatment. Such mismatches can be the result of point mutations or small deletions in the individual's Rb allele. Cleavage of the RNA strand yields two or more small RNA fragments, which run faster on the denaturing gel than the RNA probe itself, as shown in Fig. 6.

In the above RNase A technique, radiolabeled Rb gene RNA is hybridized to single strands of an individual's Rb allele which has been cloned into a vector. The RNase A technique is advantageous, however, because it also can be used without having to clone the Rb alleles. Preferably, genomic DNA is isolated from blood cells of the individual to be tested, and this genomic DNA is hybridized directly with the radiolabeled Rb RNA probes to determine sequence differences from the normal Rb gene, as follows. 5 μ g of isolated, total genomic DNA is resuspended with the labeled RNA probe in 30 μ l of hybridization buffer (80% formamide, 40mM Pipes pH6.4, 0.4M NaCl, and 1mM EDTA), and this hybridization mix is treated at 90 °C for 10 minutes to denature the DNA. The mixture then is cooled slowly to 45 °C and incubated at this temperature for 10 hours to allow hybridization of the RNA probe to the single-stranded DNA copies of the Rb allele. After hybridization, the RNase A treatment and electrophoresis are performed as above. Mismatches in the heteroduplexes between the RNA probe and the genomic copies of the individual's Rb alleles are readily detected.

Example 3: Production of Rb protein

Another use for the cloned cDNA of the normal Rb gene, as represented by p4.7R, is to produce the Rb protein. The Rb protein is produced by cloning the Rb cDNA from p4.7R into an appropriate mammalian expression vector, expressing the Rb protein from this vector in an *in vivo* expression system, and isolating the Rb protein from the medium or cells of the expression system. General *in vitro* expression vectors and systems are well known in the art.

Example 4: Immunodiagnosis

The Rb protein, produced as described above, is injected into a rabbit to produce anti-Rb antibody, which then is labeled, e.g., radioactively, fluorescently, or with an enzyme such as alkaline phosphatase. The labeled antibody is used to determine whether human tumors are of defective Rb gene origin. This can be carried out using any conventional technique. For example, the tumor sample can be liquified and tested against the labeled antibody using a conventional ELISA format. Alternatively, a tumor section can be fixed and reacted with labeled antibody, and any immune complexes then can be detected by autoradiography or fluorescence microscopy, depending on the type of label on the antibody. Tumors lacking an antigen reactive with the antibody to the Rb gene product are due to mutations of the retinoblastoma gene. Since the tumors known to be caused by a mutant Rb gene are few (including retinoblastoma and osteosarcoma), the differential diagnosis of tumors deficient in the Rb gene product is greatly limited by such a test.

Deposits

The plasmids p2AR3.8 and p2AR0.9 were deposited on July 17, 1987 with the American Type Culture Collection, Rockville, Maryland, and assigned ATCC accession numbers 40,241 and 40,242, respectively.

Other embodiments are within the following claims.

Claims

**Claims for the following Contracting States :
BE, CH, DE, FR, GB, GR, IT, LI, LU, NL, SE**

1. The use of genetic material corresponding to a normal human retinoblastoma gene or a unique subregion thereof in the preparation of material for use in a method of screening human patients for defective retinoblastoma alleles which method comprises comparing the DNA of pa-

tients with the gene or subregion.

2. The use claimed in claim 1 wherein the comparison is carried out by DNA hybridization.
3. The use claimed in claim 1 wherein the comparison is carried out by sequence comparison or sequence analysis.
4. The use claimed in claim 1 wherein the comparison is carried out by detection of mismatches in a heteroduplex between the patient's DNA and the normal gene or RNA transcripts from the normal gene.
5. A vector comprising genetic material corresponding to a normal human retinoblastoma gene, or a unique subregion thereof.
6. A vector as claimed in claim 5, wherein the subregion is at least 20 bp in length.
7. A method of detecting the presence, in a tumour sample, of a retinoblastoma protein the absence of which is associated with a neoplasm, the method comprising producing an antibody to the retinoblastoma protein, contacting the antibody with the tumour sample, and detecting immune complexes as an indication of the presence in the tumour sample of the protein.
8. A method of screening a human patient for the presence of a defective retinoblastoma (Rb) gene, the method comprising comparing the DNA of a patient with a normal human retinoblastoma gene or a unique subregion thereof.
9. A method according to claim 8 wherein the comparison is carried out by DNA hybridisation or by sequence comparison or analysis.
10. A method according to claim 8 wherein the comparison is carried out by detection of mismatches in a heteroduplex between the patient's DNA and the normal gene or RNA transcripts from the normal gene.

**Claims for the following Contracting States :
AT, ES**

1. The use of genetic material corresponding to a normal human retinoblastoma gene or a unique subregion thereof in the preparation of material for use in a method of screening human patients for defective retinoblastoma alleles which method comprises comparing the DNA of pa-

tients with the gene or subregion.

2. The use claimed in claim 1 wherein the comparison is carried out by DNA hybridization.
3. The use claimed in claim 1 wherein the comparison is carried out by sequence comparison or sequence analysis.
4. The use claimed in claim 1 wherein the comparison is carried out by detection of mismatches in a heteroduplex between the patient's DNA and the normal gene or RNA transcripts from the normal gene.
5. A process for the preparation of a vector comprising genetic material corresponding to a normal human retinoblastoma gene, or a unique subunit thereof, the process comprising either linking successive nucleotides together and/or ligating poly- and/or oligo- nucleotides.
6. A process as claimed in claim 6, wherein the subregion is at least 20 bp in length.
7. A method of detecting the presence, in a tumour sample, of a retinoblastoma protein the absence of which is associated with a neoplasm, the method comprising producing an antibody to the retinoblastoma protein, contacting the antibody with the tumour sample, and detecting immune complexes as an indication of the presence in the tumour sample of the protein.
8. A method of screening a human patient for the presence of a defective retinoblastoma (Rb) gene, the method comprising comparing the DNA of a patient with a normal human retinoblastoma gene or a unique subregion thereof.
9. A method according to claim 8 wherein the comparison is carried out by DNA hybridisation or by sequence comparison or analysis.
10. A method according to claim 8 wherein the comparison is carried out by detection of mismatches in a heteroduplex between the patient's DNA and the normal gene or RNA transcripts from the normal gene.

Patentansprüche

Patentansprüche für folgende Vertragsstaaten : BE, CH, DE, FR, GB, GR, IT, LI, LU, NL, SE

1. Verwendung von genetischem Material, das einem normalen menschlichen Retinoblastom-

- gen oder einem eindeutigen Teilbereich davon entspricht, zur Herstellung von Material zur Verwendung in einem Verfahren zum Überprüfen menschlicher Patienten auf defekte Retinoblastomallele, wobei das Verfahren den Vergleich der Patienten-DNA mit dem Gen oder Teilbereich umfaßt.
2. Verwendung nach Anspruch 1, wobei der Vergleich durch DNA-Hybridisierung durchgeführt wird. 10
 3. Verwendung nach Anspruch 1, wobei der Vergleich durch Sequenzvergleich oder Sequenzanalyse durchgeführt wird. 15
 4. Verwendung nach Anspruch 1, wobei der Vergleich durch den Nachweis von Fehlpaarungen in einem Heteroduplex zwischen der Patienten-DNA und dem normalen Gen oder RNA-Transkripten von dem normalen Gen durchgeführt wird. 20
 5. Vektor umfassend genetisches Material, das einem normalen menschlichen Retinoblastomgen oder einem eindeutigen Teilbereich davon entspricht. 25
 6. Vektor nach Anspruch 5, wobei der Teilbereich mindestens 20 bp lang ist. 30
 7. Verfahren zum Nachweis eines Retinoblastomproteins in einer Tumorprobe, wobei die Abwesenheit des Proteins mit einem Neoplasma einhergeht und das Verfahren die Herstellung eines Antikörpers gegen das Retinoblastomprotein, das Inkontaktbringen des Antikörpers mit der Tumorprobe und den Nachweis von Immunkomplexen als Anzeichen des Vorhandenseins des Proteins in der Tumorprobe umfaßt. 40
 8. Verfahren zum Überprüfen eines menschlichen Patienten auf das Vorhandensein eines defekten Retinoblastom (Rb)-gens, das den Vergleich der Patienten-DNA mit einem normalen menschlichen Retinoblastomgen oder einem eindeutigen Teilbereich davon umfaßt. 45
 9. Verfahren nach Anspruch 8, wobei der Vergleich durch DNA-Hybridisierung oder durch Sequenzvergleich oder -analyse durchgeführt wird. 50
 10. Verfahren nach Anspruch 8, wobei der Vergleich durch den Nachweis von Fehlpaarungen in einem Heteroduplex zwischen der Patienten-DNA und dem normalen Gen oder RNA-Transkripten von dem normalen Gen durchgeführt wird. 55
- kripten von dem normalen Gen durchgeführt wird.
- Patentansprüche für folgende Vertragsstaaten : AT, ES**
1. Verwendung von genetischem Material, das einem normalen menschlichen Retinoblastomgen oder einem eindeutigen Teilbereich davon entspricht, zur Herstellung von Material zur Verwendung in einem Verfahren zum Überprüfen menschlicher Patienten auf defekte Retinoblastomallele, wobei das Verfahren den Vergleich der Patienten-DNA mit dem Gen oder Teilbereich umfaßt.
 2. Verwendung nach Anspruch 1, wobei der Vergleich durch DNA-Hybridisierung durchgeführt wird.
 3. Verwendung nach Anspruch 1, wobei der Vergleich durch Sequenzvergleich oder Sequenzanalyse durchgeführt wird.
 4. Verwendung nach Anspruch 1, wobei der Vergleich durch den Nachweis von Fehlpaarungen in einem Heteroduplex zwischen der Patienten-DNA und dem normalen Gen oder RNA-Transkripten von dem normalen Gen durchgeführt wird.
 5. Verfahren zur Herstellung eines Vektors, der genetisches Material umfaßt, das einem normalen menschlichen Retinoblastomgen oder einem eindeutigen Teilbereich davon entspricht, das entweder die Verknüpfung von aufeinanderfolgenden Nucleotiden und/oder die Ligierung von Poly- und/oder Oligonucleotiden umfaßt.
 6. Verfahren nach Anspruch 5, wobei der Teilbereich mindestens 20 bp lang ist.
 7. Verfahren zum Nachweis eines Retinoblastomproteins in einer Tumorprobe, wobei die Abwesenheit des Proteins mit einem Neoplasma einhergeht und das Verfahren die Herstellung eines Antikörpers gegen das Retinoblastomprotein, das Inkontaktbringen des Antikörpers mit der Tumorprobe und den Nachweis von Immunkomplexen als Anzeichen des Vorhandenseins des Proteins in der Tumorprobe umfaßt.
 8. Verfahren zum Überprüfen eines menschlichen Patienten auf das Vorhandensein eines defekten Retinoblastom (Rb)-gens, das den Vergleich der Patienten-DNA mit einem normalen

menschlichen Retinoblastomen oder einem eindeutigen Teilbereich davon umfaßt.

9. Verfahren nach Anspruch 8, wobei der Vergleich durch DNA-Hybridisierung oder durch Sequenzvergleich oder -analyse durchgeführt wird.
10. Verfahren nach Anspruch 8, wobei der Vergleich durch den Nachweis von Fehlpaarungen in einem Heteroduplex zwischen der Patienten-DNA und dem normalen Gen oder RNA-Transkripten von dem normalen Gen durchgeführt wird.

Revendications

Revendications pour les Etats contractants suivants : BE, CH, DE, FR, GB, GR, IT, LI, LU, NL, SE

1. Utilisation du matériel génétique correspondant au gène du rétinoblastome humain normal, ou à une sous-région unique de celui-ci, dans la préparation d'un matériel destiné à être utilisé dans un procédé de dépistage, chez des patients humains, d'allèles déficients du rétinoblastome, lequel procédé comprend la comparaison de l'ADN des patients avec le gène ou la sous-région.
2. Utilisation selon la revendication 1, dans laquelle la comparaison est effectuée par hybridation d'ADN.
3. Utilisation selon la revendication 1, dans laquelle la comparaison est effectuée par comparaison des séquences ou analyse des séquences.
4. Utilisation selon la revendication 1, dans laquelle la comparaison est effectuée par détection d'erreurs d'appariement dans un hétéroduplex entre l'ADN du patient et le gène normal ou les produits de transcription d'ARN provenant du gène normal.
5. Vecteur comprenant le matériel génétique correspondant au gène du rétinoblastome humain normal, ou à une sous-région unique de celui-ci.
6. Vecteur selon la revendication 5, dans lequel la sous-région est d'une longueur d'au moins 20 paires de bases.
7. Procédé de détection de la présence, dans un échantillon tumoral, d'une protéine du rétinoblastome dont l'absence est associée à un

néoplasme, le procédé comprenant la production d'un anticorps dirigé contre la protéine du rétinoblastome, la mise en contact de l'anticorps avec l'échantillon tumoral, et la détection des complexes immuns en tant qu'indication de la présence de la protéine dans l'échantillon tumoral.

8. Procédé de dépistage chez un patient humain de la présence d'un gène déficient du rétinoblastome (Rb), le procédé comprenant la comparaison de l'ADN d'un patient avec le gène du rétinoblastome humain normal ou une sous-région unique de celui-ci.

9. Procédé selon la revendication 8, dans lequel la comparaison est effectuée par hybridation d'ADN ou par comparaison des séquences ou analyse des séquences.

10. Procédé selon la revendication 8, dans lequel la comparaison est effectuée par détection d'erreurs d'appariement dans un hétéroduplex entre l'ADN du patient et le gène normal ou les produits de transcription d'ARN provenant du gène normal.

Revendications pour les Etats contractants suivants : AT, ES

1. Utilisation du matériel génétique correspondant au gène du rétinoblastome humain normal, ou à une sous-région unique de celui-ci, dans la préparation d'un matériel destiné à être utilisé dans un procédé de dépistage, chez des patients humains, d'allèles déficients du rétinoblastome, lequel procédé comprend la comparaison de l'ADN des patients avec le gène ou la sous-région.
2. Utilisation selon la revendication 1, dans laquelle la comparaison est effectuée par hybridation d'ADN.
3. Utilisation selon la revendication 1, dans laquelle la comparaison est effectuée par comparaison des séquences ou analyse des séquences.
4. Utilisation selon la revendication 1, dans laquelle la comparaison est effectuée par détection d'erreurs d'appariement dans un hétéroduplex entre l'ADN du patient et le gène normal ou les produits de transcription d'ARN provenant du gène normal.
5. Procédé de préparation d'un vecteur comprenant le matériel génétique correspondant au

gène du rétinoblastome humain normal, ou à une sous-unité unique de celui-ci, le procédé comprenant ou bien la liaison de nucléotides successifs ensemble et/ou la soudure de poly-et/ou oligonucléotides.

5

6. Procédé selon la revendication 6, dans lequel la sous-région est d'une longueur d'au moins 20 paires de bases.

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7. Procédé de détection de la présence, dans un échantillon tumoral, d'une protéine du rétinoblastome dont l'absence est associée à un néoplasme, le procédé comprenant la production d'un anticorps dirigé contre la protéine du rétinoblastome, la mise en contact de l'anticorps avec l'échantillon tumoral, et la détection des complexes immuns en tant qu'indication de la présence de la protéine dans l'échantillon tumoral.

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8. Procédé de dépistage chez un patient humain de la présence d'un gène déficient du rétinoblastome (Rb), le procédé comprenant la comparaison de l'ADN d'un patient avec le gène du rétinoblastome humain normal ou une sous-région unique de celui-ci.

25

9. Procédé selon la revendication 8, dans lequel la comparaison est effectuée par hybridation d'ADN ou par comparaison des séquences ou analyse des séquences.

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10. Procédé selon la revendication 8, dans lequel la comparaison est effectuée par détection d'erreurs d'appariement dans un hétéroduplex entre l'ADN du patient et le gène normal ou les produits de transcription d'ARN provenant du gène normal.

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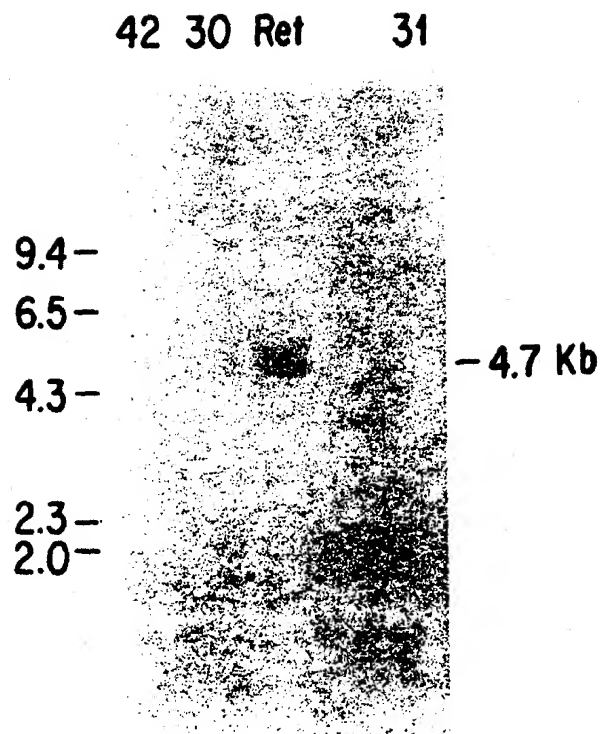


FIG. I

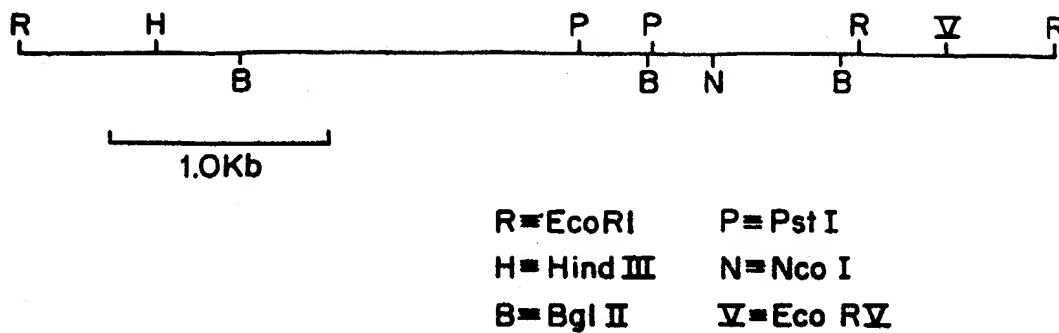


FIG. 2

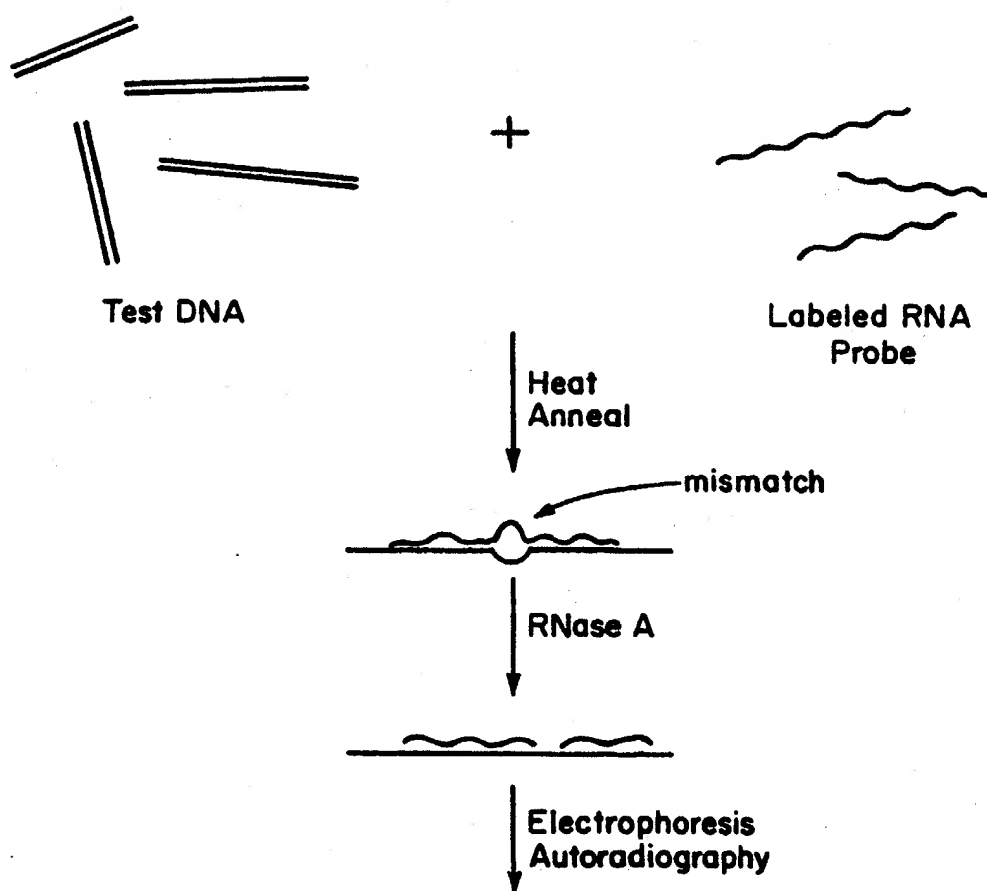


FIG. 5

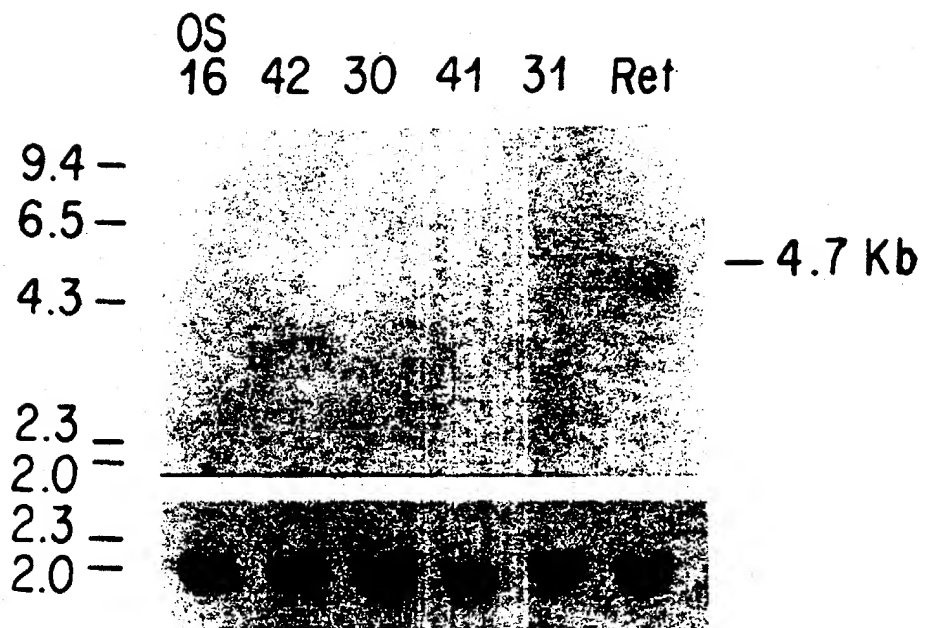


FIG. 3

FIG. 4

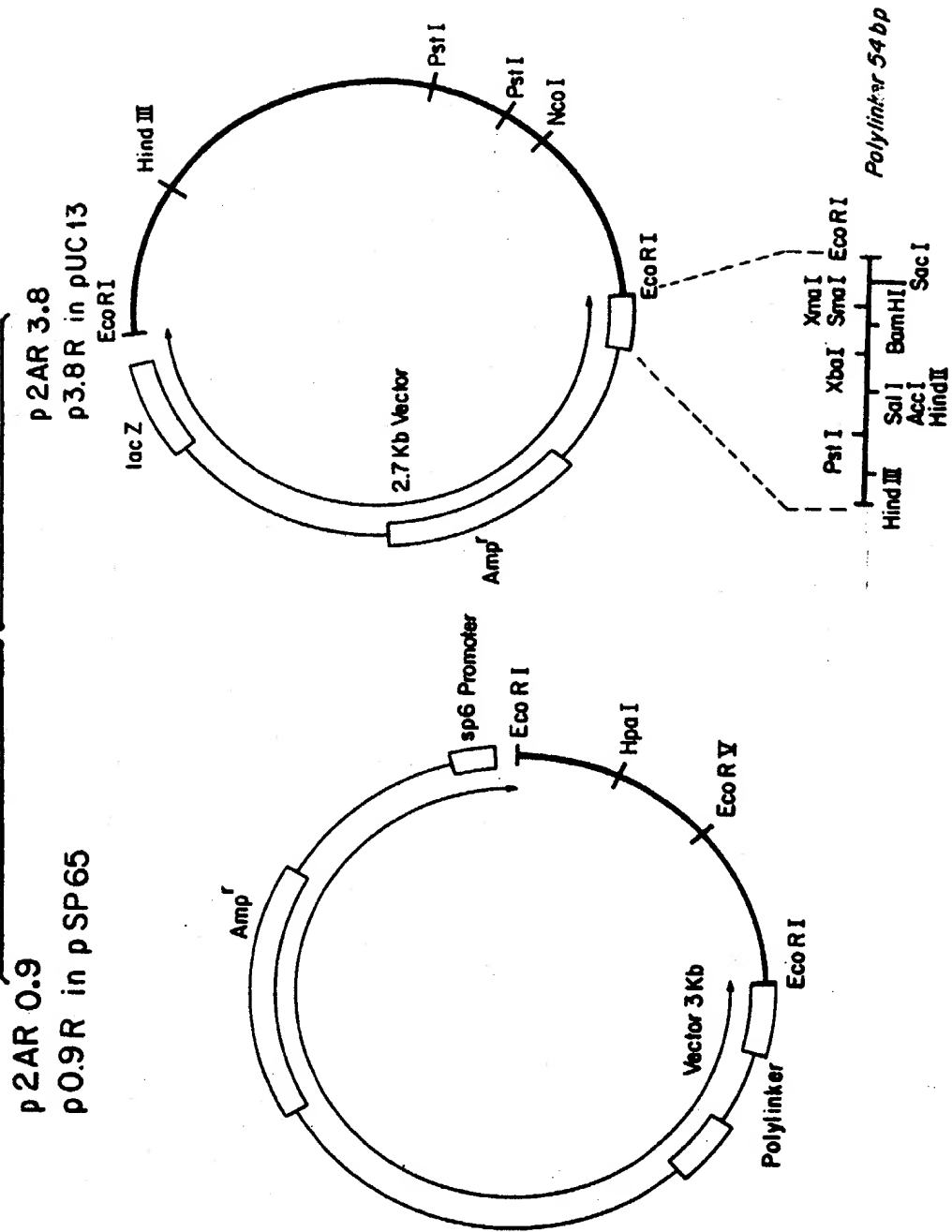


FIG. 6

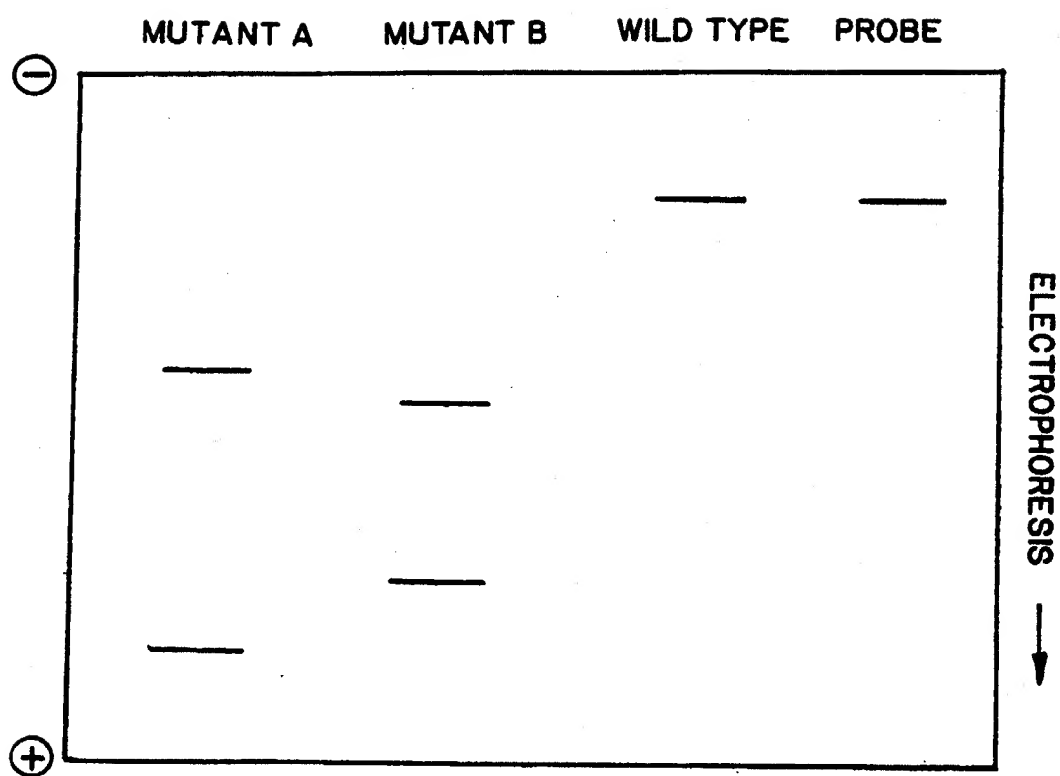


FIG. 7-1

10	20	30	40	50	60
GTC	ATG	CCG	CCC	AAA	ACC
CCC	CGA	AAA	ACG	GCC	GCC
ACC	GCC	GCT	GCC	GCC	GCG
GAA					
130	140	150	160	170	180
GAC	CTG	CCT	CTC	GTC	AGG
CTT	GAG	TTT	GAA	GAA	ACA
GAA	GAA	CCT	GAT	TTT	ACT
GCA	TTA				
190	200	210	220	230	240
TGT	CAG	AAA	TTA	AAG	ATA
CCA	GAT	CAT	GTC	AGA	GAG
AGA	GCT	TGG	TTA	ACT	TGG
GAG	AAA				
250	260	270	280	290	300
GTT	TCA	TCT	GTG	GAT	GGA
GTA	TTG	GGA	GGT	TAT	ATT
CAA	AAG	AAA	AAG	GAA	CTG
TGG	GGA				
310	320	330	340	350	360
ATC	TGT	ATC	TTT	ATT	GCA
GCA	GTT	GAC	CTA	GAT	GAG
ATG	TCG	TTC	ACT	TTT	ACT
GAG	CTA				
370	380	390	400	410	420
CAG	AAA	AAC	ATA	GAA	ATC
AGT	GTC	CAT	AAA	TTC	TTT
AAC	TTA	CTA	AAA	GAA	ATT
GAT	ACC				
430	440	450	460	470	480
AGT	ACC	AAA	GTT	GAT	AAT
GCT	ATG	TCA	AGA	CTG	TTG
AAG	AAG	TAT	GAT	GTA	TTG
TTT	GCA				
490	500	510	520	530	540
CTC	TTC	AGC	AAA	TTG	GAA
AGG	ACA	TGT	GAA	CTT	ATA
TAT	TTG	ACA	CAA	CCC	AGC
AGT	TCG				
550	560	570	580	590	600
ATA	TCT	ACT	GAA	ATA	AAT
TCT	GCA	TTG	GTG	CTA	AAA
GTT	TCT	TGG	ATC	ACA	TTT
TTA	TTA				
610	620	630	640	650	660
GCT	AAA	GGG	GAA	GTA	TTA
CAA	ATG	GAA	GAT	GAT	CTG
GTG	ATT	TCA	TTT	CAG	TTA
ATG	CTA				
670	680	690	700	710	720
TGT	GTC	CTT	GAC	TAT	TTT
ATT	AAA	CTC	TCA	CCT	CCC
ATG	TTG	CTC	AAA	GAA	CCA
TAT	AAA				
730	740	750	760	770	780
ACA	GCT	GTT	ATA	CCC	ATT
AAT	GGT	TCA	CCT	CGA	ACA
CCC	AGG	CGA	GGT	CAG	AAC
AGG	AGT				

FIG. 7-2

790	800	810	820	830	840
GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA					
A R I A K Q L E N D T R I I E V L C K E					
850	860	870	880	890	900
CAT GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG					
H E C N I D E V K N V Y F K N F I P F M					
910	920	930	940	950	960
AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA					
N S L G L V T S N G L P E V E N L S K R					
970	980	990	1000	1010	1020
TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT GAT					
Y E E I Y L K N K D L D A R L F L D H D					
1030	1040	1050	1060	1070	1080
AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT					
K T L Q T D S I D S F E T Q R T P R K S					
1090	1100	1110	1120	1130	1140
AAC CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC					
N L D E E V N V I P P H T P V R T V M N					
1150	1160	1170	1180	1190	1200
ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT CTG					
T I Q Q L M M I L N S A S D Q P S E N L					
1210	1220	1230	1240	1250	1260
ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG AAG					
I S Y F N N C T V N P K E S I L K R V K					
1270	1280	1290	1300	1310	1320
GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA					
D I G Y I F K E K F A K A V G Q G C V E					
1330	1340	1350	1360	1370	1380
ATT GGA TCA CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG					
I G S Q R Y K L G V R L Y Y R V M E S M					
1390	1400	1410	1420	1430	1440
CTT AAA TCA GAA GAA GAA CTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC AAC					
L K S E E E R L S I Q N F S K L L N D N					

FIG. 7-3

1450	1460	1470	1480	1490	1500
ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA TAT AGC AGA					
I F H M S L L A C A L E V V M A T Y S R					
1510	1520	1530	1540	1550	1560
AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG					
S T S Q N L D S G T D L S F P W I L N V					
1570	1580	1590	1600	1610	1620
CTT AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC					
L N L K A F D F Y K V I E S F I K A E G					
1630	1640	1650	1660	1670	1680
AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA TCC					
N L T R E M I K H L E R C E H R I M E S					
1690	1700	1710	1720	1730	1740
CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG GAC CGA GAA					
L A W L S D S P L F D L I K Q S K D R E					
1750	1760	1770	1780	1790	1800
GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC					
G P T D H L E S A C P L N L P L Q N N H					
1810	1820	1830	1840	1850	1860
ACT GCA GCA GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG					
T A A D M Y L S P V R S P K K K G S T T					
1870	1880	1890	1900	1910	1920
CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG					
R V N S T A N A E T Q A T S A F Q T Q K					
1930	1940	1950	1960	1970	1980
CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT CTC					
P L K S T S L S L F Y K K V Y R L A Y L					
1990	2000	2010	2020	2030	2040
CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC					
R L N T L C E R L L S E H P E L E H I I					
2050	2060	2070	2080	2090	2100
TGG ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AAG CAT TTG					
W T L F Q H T L Q N E Y E L M R D R H L					
2110	2120	2130	2140	2150	2160
GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA					
D Q I M M C S M Y G I C K V K N I D L K					
2170	2180	2190	2200	2210	2220
TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA					
F K I I V T A Y K D L P H A V Q E T F K					
2230	2240	2250	2260	2270	2280
CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC					
R V L I K E E E Y D S I I V F Y N S V F					

FIG. 7-4

2290	2300	2310	2320	2330	2340
ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA					
M Q R L K T N I L Q Y A S T R P P T L S					
2350	2360	2370	2380	2390	2400
CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT					
P I P H I P R S P Y K F P S S P L R I P					
2410	2420	2430	2440	2450	2460
GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG CCA					
G G N I Y I S P L K S P Y K I S E G L P					
2470	2480	2490	2500	2510	2520
ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG					
T P T K M T P R S R I L V S I G E S F G					
2530	2540	2550	2560	2570	2580
ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA					
T S E K F Q K I N Q M V C N S D R V L K					
2590	2600	2610	2620	2630	2640
AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA					
R S A E G S N P P K P L K K L R F D I E					
2650	2660	2670	2680	2690	2700
GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG AAA					
G S D E A D G S K H L P G E S K F Q Q K					
2710	2720	2730	2740	2750	2760
CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG					
L A E M T S T R T R M Q K Q K M N D S M					
2770	2780	2790	2800	2810	2820
GAT ACC TCA AAC AAG GAA GAG AAA TGA GGA TCT CAG GAC CTT GGT GGA CAC TGT GTA CAC					
D T S N K E E K -					
2830	2840	2850	2860	2870	2880
CTC TGG ATT CAT TGT CTC TCA CAG ATG TGA CTG TAT AAC TTT CCC AGG TTC TGT TTA TGG					
2890	2900	2910	2920	2930	2940
CCA CAT TTA ATA TCT TCA GCT CTT TTT GTG GAT ATA AAA TGT GCA GAT GCA ATT GTT TGG					
2950	2960	2970	2980	2990	3000
GTG ATT CCT AAG CCA CTT GAA ATG TTA GTC ATT GTT ATT TAT ACA AGA TTG AAA ATC TTG					
3010	3020	3030	3040	3050	3060

FIG. 7-5

TGT AAA TCC TGC CAT TTA AAA AGT TGT AGC AGA TTG TTT CCT CTT CCA AAG TAA AAT TGC
 3070 3080 3090 3100 3110 3120
 * * * * * *
 TGT GCT TTA TGG ATA GTA AGA ATG GCC CTA GAG TGG GAG TCC TGA TAA CCC AGG CCT GTC
 3130 3140 3150 3160 3170 3180
 * * * * * *
 TGA CTA CTT TGC CTT CTT TTG TAG CAT ATA GGT GAT GTT TGC TCT TGT TTT TAT TAA TTT
 3190 3200 3210 3220 3230 3240
 * * * * * *
 ATA TGT ATA TTT TTT TAA TTT AAC ATG AAC ACC CTT AGA AAA TGT GTC CTA TCT ATC TTC
 3250 3260 3270 3280 3290 3300
 * * * * * *
 CAA ATG CAA TTT GAT TGA CTG CCC ATT CAC CAA AAT TAT CCT GAA CTC TTC TGC AAA AAT
 3310 3320 3330 3340 3350 3360
 * * * * * *
 GGA TAT TAT TAG AAA TTA GAA AAA AAT TAC TAA TTT TAC ACA TTA GAT TTT ATT TTA CTA
 3370 3380 3390 3400 3410 3420
 * * * * * *
 TTG GAA TCT GAT ATA CTG TGT GCT TGT TTT ATA AAA TTT TGC TTT TAA TTA AAT AAA AGC
 3430 3440 3450 3460 3470 3480
 * * * * * *
 TGG AAG CAA AGT ATA ACC ATA TGA TAC TAT CAT ACT ACT GAA ACA GAT TTC ATA CCT CAG
 3490 3500 3510 3520 3530 3540
 * * * * * *
 AAT GTA AAA GAA CTT ACT GAT TAT TTT CTT CAT CCA ACT TAT GTT TTT AAA TGA GGA TTA
 3550 3560 3570 3580 3590 3600
 * * * * * *
 TTG ATA GTA CTC TTG GTT TTT ATA CCA TTC AGA TCA CTG AAT TTA TAA AGT ACC CAT CTA
 3610 3620 3630 3640 3650 3660
 * * * * * *
 GTA CTT GAA AAA GTA AAG TGT TCT GCC AGA TCT TAG GTA TAG AGG ACC CTA ACA CAG TAT
 3670 3680 3690 3700 3710 3720
 * * * * * *
 ATC CCA AGT GCA CTT TCT AAT GTT TCT GGG TCC TGA AGA ATT AAG ATA CAA ATT AAT TTT
 3730 3740 3750 3760 3770 3780
 * * * * * *
 ACT CCA TAA ACA GAC TGT TAA TTA TAG GAG CCT TAA TTT TTT TTT CAT AGA GAT TTG TCT
 3790 3800 3810 3820 3830 3840
 * * * * * *
 AAT TGC ATC TCA AAA TTA TTC TCC CCT CCT TAA TTT GGG AAG GTT TGT GTT TTC TCT GGA

FIG. 7-6

3850	3860	3870	3880	3890	3900
*	*	*	*	*	*
ATG GTA CAT GTC TTC CAT GTA TCT TTT GAA CTG GCA ATT GTC TAT TTA TCT TTT ATT TTT					
3910	3920	3930	3940	3950	3960
*	*	*	*	*	*
TTA AGT CAG TAT GGT CTA ACA CTG GCA TGT TCA AAG CCA CAT TAT TTC TAG TCC AAA ATT					
3970	3980	3990	4000	4010	4020
*	*	*	*	*	*
ACA AGT AAT CAA GGG TCA TTA TGG GTT AGG CAT TAA TGT TTC TAT CTG ATT TTG TGC AAA					
4030	4040	4050	4060	4070	4080
*	*	*	*	*	*
AGC TTC AAA TTA AAA CAG CTG CAT TAG AAA AAG AGG CGC TTC TCC CCT CCC CTA CAC CTA					
4090	4100	4110	4120	4130	4140
*	*	*	*	*	*
AAG GTG TAT TTA AAC TAT CTT GTG TGA TTA ACT TAT TTA GAG ATG CTG TAA CTT AAA ATA					
4150	4160	4170	4180	4190	4200
*	*	*	*	*	*
GGG GAT ATT TAA GGT AGC TTC AGC TAG CTT TTA GGA AAA TCA CTT TGT CTA ACT CAG AAT					
4210	4220	4230	4240	4250	4260
*	*	*	*	*	*
TAT TTT TAA AAA GAA ATC TGG TCT TGT TAG AAA ACA AAA TTT TAT TTT GTG CTC ATT TAA					
4270	4280	4290	4300	4310	4320
*	*	*	*	*	*
GTT TCA AAC TTA CTA TTT TGA CAG TTA TTT TGA TAA CAA TGA CAC TAG AAA ACT TGA CTC					
4330	4340	4350	4360	4370	4380
*	*	*	*	*	*
CAT TTC ATC ATT GTT TCT GCA TGA ATA TCA TAC AAA TCA GTT AGT TTT TAG GTC AAG GGC					
4390	4400	4410	4420	4430	4440
*	*	*	*	*	*
TTA CTA TTT CTG GGT CTT TTG CTA CTA AGT TCA CAT TAG AAT TAG TGC CAG AAT TTT AGG					
4450	4460	4470	4480	4490	4500
*	*	*	*	*	*
AAC TTC AGA GAT CGT GTA TTG AGA TTT CTT AAA TAA TGC TTC AGA TAT TAT TGC TTT ATT					
4510	4520	4530	4540	4550	4560
*	*	*	*	*	*
GCT TTT TTG TAT TGG TTA AAA CTG TAC ATT TAA AAT TGC TAT GTT ACT ATT TTC TAC AAT					
4570	4580	4590			
*	*	*			
TAA TAG TTT GTC TAT TTT AAA ATA AAT TAG TTG TTA G					